

1 100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700

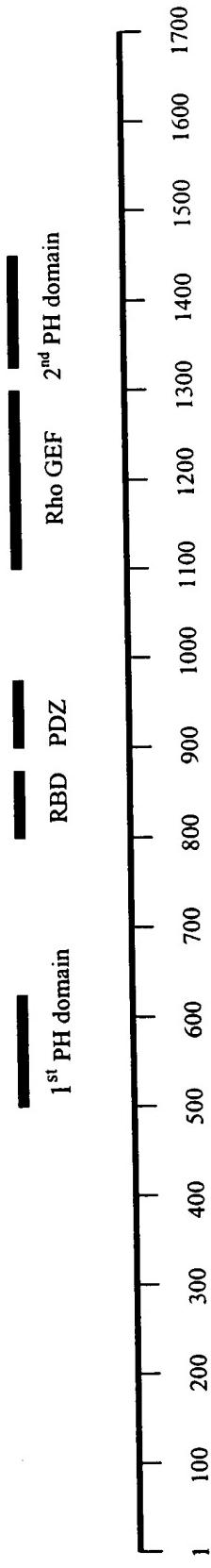


FIG. 1

PH: domain 1 of 2, from 507 to 620: score 65.9, E = 4.1e-17
*->vikeGwLlkks.....kswkRyfvLfnnvLlyykds
v + GwL+ k + +++++ + + +wk+++++L++ +Ll+y+
33521 507 VRRAGWLFFKPltvqkerklelvarRKWKQYWVTLKGCTL LFYETY 553

k.....kkpkgsipLsgcqvek.pd....kncFeirt.dr.tlllqae
++++ ++++ p+ + + + + v p + + + + + n + F + + + + + + + l + q a +
33521 554 GknsmdqssAPRCALFAEDSIVQSvPEhpkkENVFCLSNsFGdVYLFQAT 603

seeerkeWvkaiqsair<-* (SEQ ID NO:4)
s+ + + Wv+a +sa++
33521 604 SQTDLENWVTAVHSACA 620

FIG. 2A

RBD: domain 1 of 1, from 810 to 873: score -3.0, E = 2.3
*->ktirvhLPnnqrsVvevRpGmtvrDaLakalkkRGLnpsacvVrrsg
+ vh +n ++V +p +v+D+L a+k+R+L ps +
33521 810 IQTYVHFQDNHGVTVGIKPEHRVEDILTLACKMRQLEPSHYGLQ--- 853

dpqeGekkpLdldtdissLpgPeElvvEnl<-* (SEQ ID NO:5)
L+ d + + +p+P +E
33521 854 -----LRKLVDDNVEYCIPAP----YEYM 873

FIG. 2B

PDZ: domain 1 of 1, from 890 to 975: score 33.5, E = 4.8e-06
*->eitlekevkrgglGfsikggsdk.....givvsevlpGsgaAeagGr
+++l k + +Gf + + d++++ + i++s+vlp+ g A G
33521 890 DVQLTKTGSVCFGFAVTAQVDERqhlsRIFISDVLPD-GLAYGEG- 934

LkeGDvI1svNGqdvenmsheravlaikgsgg.evtLtv1Rd<-*(SEQ ID NO:6)
L++G I+ NG+ v+++ ++++++a+ + ++ +tL +++
33521 935 LRKGNEIMTLNGEAVSDL-DLKQMEALFSEKSvGLTLIARPP 975

FIG. 2C

RhoGEF: domain 1 of 1, from 1103 to 1292: score 147.0, E = 3.3e-40
*->vlkElleTEkkYvrdLeildnvymkpLreaaiisskpvltpddietiF
v+ El+ TEk Yv+dL l y++pL+++ +lt+d++e++F
33521 1103 VIQELVDTEKSYVKDLSCLFELYLEPLQNET-----FLTQDEMESLF 1144

sNiediyefhreFLkssLearisssqfedlDe....kkiepsaprlGdlF
+ +++ +ef++ FL Let is+s d + +++ + 1G F
33521 1145 GSLPEMLEFQKVFLE-TLEDGISAS--SDFNTletpSQFRKLLFSLGGSF 1191

1klkepflqvYgeYcsnkpyAqelleklrqaasnpqFaefldeveassnt
l + ++ +++Y +c+n+ +q++le+ a++ +F+ fld + + +
33521 1192 LYY-ADHFKLYSGFCANHIKVQKVLER--AKTDKAFLDARNPTKQH 1237

gAkddavkltLqsLLlkPvqRilrYpLLLkeLLkhtpegedqpdredLkk
tL+s+L+kPvqR+l+YpLLLkeL+++t+ +++++ L +
33521 1238 S-----STLESYLIKPVQRVLKYPLLKELVSLTDQ--ESEEHYHLTE 1278

aldlqlaksiNe<-*(SEQ ID NO:7)
al++++ +a++iNe
33521 1279 ALKAMEKVASHINE 1292

FIG. 2D

PH: domain 2 of 2, from 1353 to 1455: score 4.3, E = 8.7
*->fvLfnnvLyykdsk.....kkpkgsipLsg
fv+++ v+1 yk+ + +++ ++++++ +++++ +++k + ip+s
33521 1353 FVFKRAVILVYKENC1kkklpsnsrpahnstdldpFKFRWLIPISA 1399

cqvek.pd.....kncFeirt.dr.....tlllqaeseeerkeWvka
+qv+ + +++++ +e++++ + ++++++ + l+++++e++ vk
33521 1400 LQVRLgNPagtenNSIWEIHtKSeiegrpetIFQLCCSDSESKTNIVKV 1449

iqsair<-*(SEQ ID NO:8)
i+s+r
33521 1450 IRSILR 1455

FIG. 2E

PH_update: domain 1 of 2, from 507 to 622: score 63.3, E = 5.2e-15
*->vikeGwLlkks.....k.swkkryfvLfngvLlyyksk
v + GwL k + ++ ++ +++wk+++++L++ +Ll+y+
33521 507 VRRAGWLFFKPltvqkerklelvaRrKWKQYWVTLKGCTLLFYETY 553

.....kpkgsipLsgcsvre.p.....cFeivt.dr.tlllqAe
++++ ++++++p+ ++ ++ +v+ p+++++++F++++ ++++=+qA
33521 554 gknsmdqssAPRCALFAEDSIVQSvPehpkkenVFCLSNsFGdVYLFQAT 603

seeereewvealqsaika<-* (SEQ ID NO:9)
s+ ++e Wv+a +sa+a++
33521 604 SQTDLENWVTAVHSACASL 622

FIG. 3A

RBD_5: domain 1 of 1, from 810 to 881: score 68.6, E = 1.3e-16
*->ktcrvhLPdnqrtvVkvRPGktvrDaLakaLkkRgLnpeacvVrlrg
++++vh++dn +++V ++P+++v+D+L +a+k+R+L+p+++++lr+
33521 810 IQTYVHFQDNHGVTVGKPEHRVEDILTLACKMRQLEPSHYGLQLRK 856

dpqeGekkpldlnqdissLagqElvveel<-* (SEQ ID NO:10)
++ ++ + ++ ++++q +v++e+
33521 857 L---VDDNVEYCIPAPYEMQQQVYDEI 881

FIG. 3B

pdz_new: domain 1 of 1, from 900 to 976: score 39.3, E = 8.9e-08
*->gglGfsivg.....gifvssvvpGspAakaGrkslglLkvGDv
+Gf ++ + +++++ + if+s+v+p++ A+ G L++G +
33521 900 CDFGFAVTAqvderqhlsRIFISDVLPDGLAYGEG-----LRKGNE 940

IleVNGetsvegltheeavd1lkkaaggggvGekvtLtv1Rgg<-* (SEQ ID NO:11)
I+ NG + v++l+ + +l + + +tL+ +++
33521 941 IMTLNG-EAVSDLNLKQMEALFSEKSV-----GLTLIARPPD 976

FIG. 3C

RhoGEF_3: domain 1 of 1, from 1103 to 1292: score 217.7, E = 1.8e-61
 *->vlkELLqTErnYVrdLkilvevflkpLkkeakssllplspdevktl
 v++EL++TE++YV+dL +l e +l+pL++e +l++de+++1
 33521 1103 VIQELVDTEKSYVKDLSCLFELYLEPLQNET-----FLTQDEMESL 1143

FgpNieceiyefHrrFLdeLeerveewllskdl.Ksernsviedsgerigd
 Fg ++e +ef++ FL++Le+ ++ + d++ e+ s++++ +g
 33521 1144 FG-SLPEMLEFQKVLETLEDGISASS---DFnTLETPSQFRKLLFSLGG 1189

vFlklsaeeffkiYseYcsnhpdalellkkLmkkknpaFqkf1keies
 Fl + +++fk+Ys +c+nh + ++l+ +k+++aF++f1+ +
 33521 1190 SFLYY---ADHFKLYSGFCANHIKVQKVLER---AKTDKAFAFLDARNP 1233

kpncrsksearltLes1LikPvQR1t kYpLLLkellkhtppdhedredLk
 +++ tLes+LikPvQR++kYpLLLkel t+ ++e++ +L+
 33521 1234 TKQHS-----STLESYLIKPVQRVLKYPLLKELVSLTDQESEEHYHLT 1277

kAleaikelasqvNe<-* (SEQ ID NO:12)
 +Al+a++++as++Ne
 33521 1278 EALKAMEKVASHINE 1292

FIG. 3D

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PH_update: domain 2 of 2, from 1326 to 1457: score 17.7, E = 0.28
          *->vikeGwLlkks.....k.swkkryfvLfngvLyyksk.....
          +++++ +++++ + + ++ ++ fv+++ v+l yk+ + ++
33521 1326     LLMHSTVSWLNpfIsgkaRkDLELTVFVFKRAVILVYKENcklkkk 1372

          .....kpkgsipLsgcsvre.p.....cFeivt.d
          ++++++ +++++ ++ k + ips +vr + + + +++++ +e+++++
33521 1373 lpsnsrpahnstdldpfKFRWLIPISALQVRLgNpagtennsIWELIHtK 1422

          r.....tlllqAeseereeeWvealqsaaiaka<-* (SEQ ID NO:13)
          + ++++++ + l+++++e++ v+ ++s +++
33521 1423 SeiegrpetIFQLCCSDSESKTNIVKVIRSILREN      1457

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FIG. 3E